

# SEQUENCE LISTING

<110> Murphy, Erin E.  
 Mattson, Jeanine D.  
 Bates, Elizabeth Esther Mary  
 Gorman, Daniel M.  
 Lebecque, Serge J.E.

<120> Mammalian Genes; Related Reagents

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<170> PatentIn Ver. 2.0

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cca ggc ctg tgc ctg ctg tgc ctg gtg ttg gcg ctg cct gcc ctg ctg 164  
 Pro Gly Leu Ser Leu Leu Cys Leu Val Leu Ala Leu Pro Ala Leu Leu  
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ccg gtg ccg gct gta cgc gga gtg gca gaa aca ccc acc tac ccc tgg 212  
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cgg gac gca gag aca ggg gag cgg ctg gtg tgc gcc cag tgc ccc cca 260  
 Arg Asp Ala Glu Thr Gly Glu Arg Leu Val Cys Ala Gln Cys Pro Pro  
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 Gly Thr Phe Val Gln Arg Pro Cys Arg Arg Asp Ser Pro Met Thr Cys

A2  
 Cm: +

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Gly Pro Cys Pro Pro Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu			
60	65	70	75
cgc tgc cgc twc tgc tac gtc ctc tgc ggg gag cgt gag gag gag gca			404
Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly Glu Arg Glu Glu Glu Ala			
80	85		90
cgg gct tgc cac gcc acc cac aac cgt gcc tgc cgc tgc cgc acc ggc			452
Arg Ala Cys His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly			
95	100		105
ttc ttc gcg cac gct ggt ttc tgc ttg gag cac gca tgc tgt cca cct			500
Phe Phe Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro			
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ggt gcc ggc gtg att gcc ccg ggc acc ccc agc cag aac acg cag tgc			548
Gly Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys			
125	130		135
cag ccg tgc ccc cca ggc acc ttc tca gcc agc agc tcc agc tca gag			596
Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser Glu			
140	145		150
cag tgc cag ccc cac cgc aac tgc acg gcc ctg ggc ctg gcc ctc aat			644
Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala Leu Asn			
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gtg cca ggc tct tcc tcc cat gac acc ctg tgc acc agc tgc act ggc			692
Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser Cys Thr Gly			
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ttc ccc ctc agc acc agg gta cca gga gct gag gag tgt gag cgt gcc			740
Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu Cys Glu Arg Ala			
190	195		200
gtc atc gac ttt gtg gct ttc cag gac atc tcc atc aag agg ctg cag			788
Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser Ile Lys Arg Leu Gln			
205	210		215
cgg ctg ctg cag gcc ctc gag gcc ccg gag ggc tgg ggt ccg aca cca			836
Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu Gly Trp Gly Pro Thr Pro			
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agg gcg ggc cgc gcg gcc ttg cag ctg aag ctg cgt cgg cgg ctc acg			884
Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys Leu Arg Arg Arg Leu Thr			
240	245		250
gag ctc ctg ggg gcg cag gac ggg gcg ctg ctg gtg cgg ctg ctg cag			932
Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu Leu Val Arg Leu Leu Gln			
255	260		265
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Ala Leu Arg Val Ala Arg Met Pro Gly Leu Glu Arg Ser Val Arg Glu			
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A2  
Cm.t

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Asp Ser Pro Met Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln  
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Phe Trp Asn Tyr Leu Glu Arg Cys Arg Xaa Cys Tyr Val Leu Cys Gly  
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Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala  
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Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu  
 105 110 115

His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro  
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Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala  
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Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala  
 150 155 160 165

Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu  
 170 175 180

Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala  
 185 190 195

Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile  
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Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu

A2  
 cm.t

215                      220                      225  
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 Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu  
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 Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu  
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A2  
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Met Gly Thr Ser Pro  
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Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg Arg Ala  
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aca gcc acg atg atc gcg ggc tcc ctt ctc ctg ctt gga ttc ctt agc 512  
Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe Leu Ser  
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Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys Asp Lys  
15 20 25

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Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr Ser Cys  
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gcg tct gkc agc agt tgc cct gtg ggg acc ttt acc agg cat gag aat 704  
Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His Glu Asn  
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ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg cca atg 752  
Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp Pro Met  
65 70 75

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Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys Thr Cys  
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cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat acg gtg 848  
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agt gtg atg aan gca aag cat aca cag act gtc tgg atc aga acn tgg 992  
Ser Val Met Xaa Ala Lys His Thr Gln Thr Val Trp Ile Arg Xaa Trp  
145 150 155

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Cm. +

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Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys  
25 30 35

Thr Asn Thr Ser Cys Ala Ser Xaa Ser Ser Cys Pro Val Gly Thr Phe  
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Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro  
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Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp  
75 80 85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys  
90 95 100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly  
105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Tyr Phe  
120 125 130 135

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Thr Thr

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cggtttctcc ccgcctgggc ggccgcgcgc ctgggcaggt gctgagcgcc cctagcgcc 240  
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ccagctgccc cgcgcgcccc gggcgccct gcagtcgcc ggttcagcc atg ggg acc 418  
Met Gly Thr  
-40

tct ccg agc agc agc acc gcc ctc gcc tcc tgc agc cgc atc gcc cgc 466  
Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg Ile Ala Arg  
-35 -30 -25

cga gcc aca gcc acg atg atc gcg gcc tcc ctt ctc ctg ctt gga ttc 514  
Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu Leu Gly Phe  
-20 -15 -10

ctt agc acc acc aca gct cag cca gaa cag aag gcc tcg aat ctc att 562  
Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser Asn Leu Ile  
-5 -1 1 5 10

ggc aca tac cgc cat gtt gac cgt gcc acc gcc cag gtg cta acc tgt 610  
Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val Leu Thr Cys  
15 20 25

gac aag tgt cca gca gga acc tat gtc tct gag cat tgt acc aac aca 658  
Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys Thr Asn Thr  
30 35 40

agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt acc agg cat 706  
Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe Thr Arg His  
45 50 55

gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca tgc cca tgg 754  
Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro Cys Pro Trp  
60 65 70

cca atg att gag aaa tta cct tgt gct gcc ttg act gac cga gaa tgc 802  
Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp Arg Glu Cys  
75 80 85 90

act tgc cca cct ggc atg ttc cag tct aac gct acc tgt gcc ccc cat 850  
Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys Ala Pro His  
95 100 105

A2  
cm.t

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Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe Ser Asp Val  
125 130 135

cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt ctg agt cag 994  
Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys Leu Ser Gln  
140 145 150

aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac aac gtc tgt 1042  
Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp Asn Val Cys  
155 160 165

ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc cct ggc aca 1090  
Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser Pro Gly Thr  
175 180 185

gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa gtc cct tcc 1138  
Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu Val Pro Ser  
190 195 200

tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc aac tct tct 1186  
Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser Asn Ser Ser  
205 210 215

gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa ggg aca gtc 1234  
Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu Gly Thr Val  
220 225 230

cct gac aac aca agc tca gca agg ggg aag gaa gac gtg aac aag acc 1282  
Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val Asn Lys Thr  
235 240 245

ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc cac cac aga 1330  
Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro His His Arg  
255 260 265

cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg ggc gag aag 1378  
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270 275 280

tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct aga cag aac 1426  
Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro Arg Gln Asn  
285 290 295

cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg atg att gtg 1474  
Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp Met Ile Val  
300 305 310

ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc agt atc cgg 1522  
Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys Ser Ile Arg  
315 320 325 330

aaa agc tcg agg act ctg aaa aag ggg ccc cgg cag gat ccc agt gcc 1570

A2  
cm.T



Lys	Ser	Ser	Arg	Thr	Leu	Lys	Lys	Gly	Pro	Arg	Gln	Asp	Pro	Ser	Ala		
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Ile	Val	Glu	Lys	Ala	Gly	Leu	Lys	Lys	Ser	Met	Thr	Pro	Thr	Gln	Asn		
			350					355					360				
cgg	gag	aaa	tgg	atc	tac	tac	tgc	aat	ggc	cat	ggt	atc	gat	atc	ctg		1666
Arg	Glu	Lys	Trp	Ile	Tyr	Tyr	Cys	Asn	Gly	His	Gly	Ile	Asp	Ile	Leu		
		365					370					375					
aag	ctt	gta	gca	gcc	caa	gtg	gga	agc	cag	tgg	aaa	gat	atc	tat	cag		1714
Lys	Leu	Val	Ala	Ala	Gln	Val	Gly	Ser	Gln	Trp	Lys	Asp	Ile	Tyr	Gln		
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Phe	Leu	Cys	Asn	Ala	Ser	Glu	Arg	Glu	Val	Ala	Ala	Phe	Ser	Asn	Gly		
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tac	aca	gcc	gac	cac	gag	cgg	gcc	tac	gca	gct	ctg	cag	cac	tgg	acc		1810
Tyr	Thr	Ala	Asp	His	Glu	Arg	Ala	Tyr	Ala	Ala	Leu	Gln	His	Trp	Thr		
				415					420					425			
atc	cgg	ggc	ccc	gag	gcc	agc	ctc	gcc	cag	cta	att	agc	gcc	ctg	cgc		1858
Ile	Arg	Gly	Pro	Glu	Ala	Ser	Leu	Ala	Gln	Leu	Ile	Ser	Ala	Leu	Arg		
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cag	cac	cgg	aga	aac	gat	gtt	gtg	gag	aag	att	cgt	ggg	ctg	atg	gaa		1906
Gln	His	Arg	Arg	Asn	Asp	Val	Val	Glu	Lys	Ile	Arg	Gly	Leu	Met	Glu		
			445				450					455					
gac	acc	acc	cag	ctg	gaa	act	gac	aaa	cta	gct	ctc	ccg	atg	agc	ccc		1954
Asp	Thr	Thr	Gln	Leu	Glu	Thr	Asp	Lys	Leu	Ala	Leu	Pro	Met	Ser	Pro		
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agc	ccg	ctt	agc	ccg	agc	ccc	atc	ccc	agc	ccc	aac	gcg	aaa	ctt	gag		2002
Ser	Pro	Leu	Ser	Pro	Ser	Pro	Ile	Pro	Ser	Pro	Asn	Ala	Lys	Leu	Glu		
					480				485					490			
aat	tcc	gct	ctc	ctg	acg	gtg	gag	cct	tcc	cca	cag	gac	aag	aac	aag		2050
Asn	Ser	Ala	Leu	Leu	Thr	Val	Glu	Pro	Ser	Pro	Gln	Asp	Lys	Asn	Lys		
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Gly	Phe	Phe	Val	Asp	Glu	Ser	Glu	Pro	Leu	Leu	Arg	Cys	Asp	Ser	Thr		
			510					515					520				
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Ser	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys		
			525				530					535					
gaa	aag	aag	gac	aca	gtg	ttg	cgg	cag	gta	cgc	ctg	gac	ccc	tgt	gac		2194
Glu	Lys	Lys	Asp	Thr	Val	Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp		
			540			545					550						
ttg	cag	cct	atc	ttt	gat	gac	atg	ctc	cac	ttt	cta	aat	cct	gag	gag		2242
Leu	Gln	Pro	Ile	Phe	Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu		
					555		560			565					570		

A2  
Cm.T

ctg cgg gtg att gaa gag att ccc cag gct gag gac aaa cta gac cgg 2290  
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cta ttc gaa att att gga gtc aag agc cag gaa gcc agc cag acc ctc 2338  
 Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu  
                     590                    595                    600

ctg gac tct gtt tat agc cat ctt cct gac ctg ctg tagaacatag 2384  
 Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
                     605                    610

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                     -25                    -20                    -15                    -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser  
                     -5                    -1                    1                    5

Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val  
                     10                    15                    20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys  
                     25                    30                    35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe  
                     40                    45                    50                    55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro  
                     60                    65                    70

A2  
 cm't

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp  
 75 80 85  
 Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys  
 90 95 100  
 Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly  
 105 110 115  
 Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe  
 120 125 130 135  
 Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys  
 140 145 150  
 Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp  
 155 160 165  
 Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser  
 170 175 180  
 Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu  
 185 190 195  
 Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser  
 200 205 210 215  
 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu  
 220 225 230  
 Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val  
 235 240 245  
 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro  
 250 255 260  
 His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly  
 265 270 275  
 Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro  
 280 285 290 295  
 Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp  
 300 305 310  
 Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys  
 315 320 325  
 Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp  
 330 335 340  
 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro  
 345 350 355  
 Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile  
 360 365 370 375

A2  
 Cmt

Asp Ile Leu Lys Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp  
 380 385 390  
 Ile Tyr Gln Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe  
 395 400 405  
 Ser Asn Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln  
 410 415 420  
 His Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser  
 425 430 435  
 Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg Gly  
 440 445 450 455  
 Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala Leu Pro  
 460 465 470  
 Met Ser Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro Ser Pro Asn Ala  
 475 480 485  
 Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro Ser Pro Gln Asp  
 490 495 500  
 Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu Pro Leu Leu Arg Cys  
 505 510 515  
 Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu Ser Arg Asn Gly Ser Phe  
 520 525 530 535  
 Ile Thr Lys Glu Lys Lys Asp Thr Val Leu Arg Gln Val Arg Leu Asp  
 540 545 550  
 Pro Cys Asp Leu Gln Pro Ile Phe Asp Asp Met Leu His Phe Leu Asn  
 555 560 565  
 Pro Glu Glu Leu Arg Val Ile Glu Glu Ile Pro Gln Ala Glu Asp Lys  
 570 575 580  
 Leu Asp Arg Leu Phe Glu Ile Ile Gly Val Lys Ser Gln Glu Ala Ser  
 585 590 595  
 Gln Thr Leu Leu Asp Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
 600 605 610

<210> 7  
 <211> 1474  
 <212> DNA  
 <213> primate

<220>  
 <221> CDS  
 <222> (1)..(1332)

<220>  
 <221> mat\_peptide  
 <222> (124)..(1332)

A2  
 Cm.†

<400> 7

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Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg  
-40 -35 -30

atc gcc cgc cga gcc aca gcc acg atg atc gcg ggc tcc ctt ctc ctg 96  
Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu  
-25 -20 -15 -10

ctt gga ttc ctt agc acc acc aca gct cag cca gaa cag aag gcc tgc 144  
Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser  
-5 -1 1 5

aat ctc att ggc aca tac cgc cat gtt gac cgt gcc acc ggc cag gtg 192  
Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val  
10 15 20

cta acc tgt gac aag tgt cca gca gga acc tat gtc tct gag cat tgt 240  
Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys  
25 30 35

acc aac aca agc ctg cgc gtc tgc agc agt tgc cct gtg ggg acc ttt 288  
Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe  
40 45 50 55

acc agg cat gag aat ggc ata gag aaa tgc cat gac tgt agt cag cca 336  
Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro  
60 65 70

tgc cca tgg cca atg att gag aaa tta cct tgt gct gcc ttg act gac 384  
Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp  
75 80 85

cga gaa tgc act tgc cca cct ggc atg ttc cag tct aac gct acc tgt 432  
Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys  
90 95 100

gcc ccc cat acg gtg tgt cct gtg ggt tgg ggt gtg cgg aag aaa ggg 480  
Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly  
105 110 115

aca gag act gag gat gtg cgg tgt aag cag tgt gct cgg ggt acc ttc 528  
Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe  
120 125 130 135

tca gat gtg cct tct agt gtg atg aaa tgc aaa gca tac aca gac tgt 576  
Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys  
140 145 150

ctg agt cag aac ctg gtg gtg atc aag ccg ggg acc aag gag aca gac 624  
Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp  
155 160 165

aac gtc tgt ggc aca ctc ccg tcc ttc tcc agc tcc acc tca cct tcc 672  
Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Ser Ser Pro Ser  
170 175 180

A2  
Cm. it

cct ggc aca gcc atc ttt cca cgc cct gag cac atg gaa acc cat gaa 720  
 Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu  
 185 190 195

gtc cct tcc tcc act tat gtt ccc aaa ggc atg aac tca aca gaa tcc 768  
 Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser  
 200 205 210 215

aac tct tct gcc tct gtt aga cca aag gta ctg agt agc atc cag gaa 816  
 Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu  
 220 225 230

ggg aca gtc cct gac aac aca agc tca gca agg ggg aag gaa gac gtg 864  
 Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val  
 235 240 245

aac aag acc ctc cca aac ctt cag gta gtc aac cac cag caa ggc ccc 912  
 Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro  
 250 255 260

cac cac aga cac atc ctg aag ctg ctg ccg tcc atg gag gcc act ggg 960  
 His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly  
 265 270 275

ggc gag aag tcc agc acg ccc atc aag ggc ccc aag agg gga cat cct 1008  
 Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro  
 280 285 290 295

aga cag aac cta cac aag cat ttt gac atc aat gag cat ttg ccc tgg 1056  
 Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp  
 300 305 310

atg att gtg ctt ttc ctg ctg ctg gtg ctt gtg gtg att gtg gtg tgc 1104  
 Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys  
 315 320 325

agt atc cgg aaa agc tgc agg act ctg aaa aag ggg ccc cgg cag gat 1152  
 Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp  
 330 335 340

ccc agt gcc att gtg gaa aag gca ggg ctg aag aaa tcc atg act cca 1200  
 Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro  
 345 350 355

acc cag aac cgg gag aaa tgg atc tac tac tgc aat ggc cat gga ccc 1248  
 Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro  
 360 365 370 375

cat gat gag gag tgg ggg ttg atg gag aga cat att caa gat att tat 1296  
 His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr  
 380 385 390

att caa aga agc aat caa gat tca gaa aga tgg ggt tgataatttt 1342  
 Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly  
 395 400

tacttcaccc tgggaggcag catagtgcag tgaaaggat cgatatcctg aagcttgtag 1402

A2  
 cm +

cagcccaagt gggaagccag tggaagata tctatcagtt tctttgcaat gccagtgaga 1462  
 gggaggttgc tg 1474

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 <211> 444  
 <212> PRT  
 <213> primate

<400> 8  
 Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser Arg  
 -40 -35 -30

Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu Leu Leu  
 -25 -20 -15 -10

Leu Gly Phe Leu Ser Thr Thr Thr Ala Gln Pro Glu Gln Lys Ala Ser  
 -5 -1 1 5

Asn Leu Ile Gly Thr Tyr Arg His Val Asp Arg Ala Thr Gly Gln Val  
 10 15 20

Leu Thr Cys Asp Lys Cys Pro Ala Gly Thr Tyr Val Ser Glu His Cys  
 25 30 35

Thr Asn Thr Ser Leu Arg Val Cys Ser Ser Cys Pro Val Gly Thr Phe  
 40 45 50 55

Thr Arg His Glu Asn Gly Ile Glu Lys Cys His Asp Cys Ser Gln Pro  
 60 65 70

Cys Pro Trp Pro Met Ile Glu Lys Leu Pro Cys Ala Ala Leu Thr Asp  
 75 80 85

Arg Glu Cys Thr Cys Pro Pro Gly Met Phe Gln Ser Asn Ala Thr Cys  
 90 95 100

Ala Pro His Thr Val Cys Pro Val Gly Trp Gly Val Arg Lys Lys Gly  
 105 110 115

Thr Glu Thr Glu Asp Val Arg Cys Lys Gln Cys Ala Arg Gly Thr Phe  
 120 125 130 135

Ser Asp Val Pro Ser Ser Val Met Lys Cys Lys Ala Tyr Thr Asp Cys  
 140 145 150

Leu Ser Gln Asn Leu Val Val Ile Lys Pro Gly Thr Lys Glu Thr Asp  
 155 160 165

Asn Val Cys Gly Thr Leu Pro Ser Phe Ser Ser Ser Thr Ser Pro Ser  
 170 175 180

Pro Gly Thr Ala Ile Phe Pro Arg Pro Glu His Met Glu Thr His Glu  
 185 190 195

Val Pro Ser Ser Thr Tyr Val Pro Lys Gly Met Asn Ser Thr Glu Ser  
 200 205 210 215

A2  
 Cmt

Asn Ser Ser Ala Ser Val Arg Pro Lys Val Leu Ser Ser Ile Gln Glu  
220 225 230

Gly Thr Val Pro Asp Asn Thr Ser Ser Ala Arg Gly Lys Glu Asp Val  
235 240 245

Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His Gln Gln Gly Pro  
250 255 260

His His Arg His Ile Leu Lys Leu Leu Pro Ser Met Glu Ala Thr Gly  
265 270 275

Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly Pro Lys Arg Gly His Pro  
280 285 290 295

Arg Gln Asn Leu His Lys His Phe Asp Ile Asn Glu His Leu Pro Trp  
300 305 310

Met Ile Val Leu Phe Leu Leu Leu Val Leu Val Val Ile Val Val Cys  
315 320 325

Ser Ile Arg Lys Ser Ser Arg Thr Leu Lys Lys Gly Pro Arg Gln Asp  
330 335 340

Pro Ser Ala Ile Val Glu Lys Ala Gly Leu Lys Lys Ser Met Thr Pro  
345 350 355

Thr Gln Asn Arg Glu Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Pro  
360 365 370 375

His Asp Glu Glu Trp Gly Leu Met Glu Arg His Ile Gln Asp Ile Tyr  
380 385 390

Ile Gln Arg Ser Asn Gln Asp Ser Glu Arg Trp Gly  
395 400

<210> 9

<211> 227

<212> PRT

<213> rodent

<400> 9

Met Ala Pro Ala Ala Leu Trp Val Ala Leu Val Phe Glu Leu Gln Leu  
1 5 10 15

Trp Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr  
20 25 30

Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp  
35 40 45

Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val  
50 55 60

Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu  
65 70 75 80

A2  
Gen 14



Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser  
85 90 95

Cys Ser Ser Ser Cys Thr Thr Asp Gln Val Glu Ile Arg Ala Cys Thr  
100 105 110

Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala  
115 120 125

Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys  
130 135 140

Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn  
145 150 155 160

Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser  
165 170 175

Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile  
180 185 190

Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr  
195 200 205

Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr  
210 215 220

Arg Ser Gln  
225

<210> 10  
<211> 225  
<212> PRT  
<213> primate

<400> 10  
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
100 105 110

A2  
omit

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
145 150- 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
210 215 220

Gln  
225

<210> 11  
<211> 187  
<212> PRT  
<213> primate

<400> 11  
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
1 5 10 15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

A2  
Cm.t

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly  
180 185

<210> 12  
<211> 636  
<212> DNA  
<213> rodent

<220>  
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<222> (104)..(553)

<220>  
<221> mat\_peptide  
<222> (191)..(553)

<400> 12  
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cagcactggc gagtagcagg aataaacacg tttggtgaga gcc atg gca ctc aag 115  
Met Ala Leu Lys

gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc cta 163  
Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe Leu  
-25 -20 -15 -10

ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg cag 211  
Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg Gln  
-5 -1 1 5

cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag tgc 259  
Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln Cys  
10 15 20

gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg gag 307  
Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly Glu  
25 30 35

gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac tgg 355  
Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp Trp  
40 45 50 55

ggg ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac cgc 403  
Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn Arg  
60 65 70

ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg gac 451  
Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly Asp  
75 80 85

A2  
Cm't

tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa gac 499  
 Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln Asp  
           90                                  95                                  100

atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca cac 547  
 Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro His  
           105                                  110                                  115

tgt gag tgatgtgccca agtggcagca gacctttaa aaaaaaagaa aaaaaaacia 603  
 Cys Glu  
 120

acaaaaacia aaaaaaaaaa aaaaaaaaaa aaa 636

<210> 13  
 <211> 150  
 <212> PRT  
 <213> rodent

<400> 13  
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala  
                                   -25                                  -20                                  -15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly  
                                   -10                                  -5                                  -1 1

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu  
           5                                  10                                  15

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe  
           20                                  25                                  30                                  35

Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe  
                                   40                                  45                                  50

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala  
                                   55                                  60                                  65

Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala  
                                   70                                  75                                  80

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val  
           85                                  90                                  95

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro  
           100                                  105                                  110                                  115

Tyr Glu Pro His Cys Glu  
                                   120

<210> 14  
 <211> 474  
 <212> DNA  
 <213> primate

<220>

A2  
 Cm.t

<221> CDS  
<222> (78)..(473)

<220>  
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<222> (308)  
<223> N; may be A, C, G, or T

<220>  
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<220>  
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<222> (333)  
<223> N; may be A, C, G, or T

<220>  
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<222> (412)  
<223> N; may be A, C, G, or T

<220>  
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<222> (431)  
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<220>  
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<222> (436)  
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<223> N; may be A, C, G, or T

<220>  
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<222> (473)  
<223> N; may be A, C, G, or T

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ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110  
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln  
1 5 10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158  
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu  
15 20 25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206  
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala  
30 35 40

A2  
Cm.t

tgc cct cct cgc agt aca aaa gca gct ggg gcc acc aca aat gtc aga 254  
 Cys Pro Pro Arg Ser Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg  
 45 50 55

gtt gca tca cct gtg ctg tca tca atc gtg ttc aga agg ttc aac tgc 302  
 Val Ala Ser Pro Val Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys  
 60 65 70 75

aca gtn acc tct nat gct gtc tgt ggg gga ngg ttt gcc caa gtt tct 350  
 Thr Xaa Thr Ser Xaa Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser  
 80 85 90

aac cga aag aca cgc cat tgg aag gct gcc agg acc aag gat ggc atc 398  
 Asn Arg Lys Thr Arg His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile  
 95 100 105

ccg tgg cac aaa gnc aga ccc cca act tct gan ggt tnc aaa gtg nct 446  
 Pro Trp His Lys Xaa Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa  
 110 115 120

ttc caa ttg gag ctt aat ggg agg can a 474  
 Phe Gln Leu Glu Leu Asn Gly Arg Xaa  
 125 130

<210> 15  
 <211> 132  
 <212> PRT  
 <213> primate

<400> 15  
 Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val  
 1 5 10 15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly  
 20 25 30

Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Ser  
 35 40 45

Thr Lys Ala Ala Gly Ala Thr Thr Asn Val Arg Val Ala Ser Pro Val  
 50 55 60

Leu Ser Ser Ile Val Phe Arg Arg Phe Asn Cys Thr Xaa Thr Ser Xaa  
 65 70 75 80

Ala Val Cys Gly Gly Xaa Phe Ala Gln Val Ser Asn Arg Lys Thr Arg  
 85 90 95

His Trp Lys Ala Ala Arg Thr Lys Asp Gly Ile Pro Trp His Lys Xaa  
 100 105 110

Arg Pro Pro Thr Ser Xaa Gly Xaa Lys Val Xaa Phe Gln Leu Glu Leu  
 115 120 125

Asn Gly Arg Xaa  
 130

A2  
 Cmut

<210> 16  
<211> 546  
<212> DNA  
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<220>  
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<222> (78)..(308)

<220>  
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<222> (317)  
<223> N; may be A, C, G, or T

<220>  
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<220>  
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<220>  
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<223> N; may be A, C, G, or T

<220>  
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<222> (429)  
<223> N; may be A, C, G, or T

<220>  
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<222> (433)  
<223> N; may be A, C, G, or T

<220>  
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<222> (452)  
<223> N; may be A, C, G, or T

<220>  
<221> misc\_feature  
<222> (468)

A2  
Cm 4

<223> N; may be A, C, G, or T

<220>

<221> misc\_feature

<222> (483)

<223> N; may be A, C, G, or T

<220>

<221> misc\_feature

<222> (534)

<223> N; may be A, C, G, or T

<220>

<221> misc\_feature

<222> (541)

<223> N; may be A, C, G, or T

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ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110  
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln  
1 5 10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158  
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu  
15 20 25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc acc gcc 206  
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala  
30 35 40

tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254  
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln  
45 50 55

agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc caa ctg 302  
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu  
60 65 70 75

cac agc taacctctna tgctgtctgt ggggatgttt gncccaagtt ctnaccgaaa 358  
His Ser

agacacgccca tgggaagggt ggcaggacca ngaatggccn tcccgtggca gaaagccaga 418

ccccccaacn nctgnagggt ccaatgtggc cttncatttt ggaagcttan tgggaaggca 478

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gcntgccca 546

<210> 17

<211> 77

<212> PRT

<213> primate

<400> 17

A2  
cm<sup>+</sup>



Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val  
1 5 10 15

Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly  
20 25 30

Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg  
35 40 45

Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys  
50 55 60

Ala Val Ile Asn Arg Val Gln Lys Val Gln Leu His Ser  
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<221> misc\_feature

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<223> N; may be A, C, G, or T

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ttaccggcct tcccacc atg gat tgc caa gaa aat gag tac tgg gac caa 110  
Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln  
1 5 10

tgg gga cgg tgt gtc acc tgc caa cgg tgt ggt cct gga cag gag cta 158  
Trp Gly Arg Cys Val Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu  
15 20 25

tcc aag gat tgt ggt tat gga gag ggt gga gat gcc tac tgc aca gcc 206  
Ser Lys Asp Cys Gly Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala  
30 35 40

tgc cct cct cgc agg tac aaa agc agc tgg ggc cac cac aaa tgt cag 254  
Cys Pro Pro Arg Arg Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln  
45 50 55

agt tgc atc acc tgt gct gtc atc aat cgt gtt cag aag gtc aac tgc 302  
Ser Cys Ile Thr Cys Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys  
60 65 70 75

aca gct acc tct aat gct gtc tgt ggg gac tgt ttg ccc agg ttc tac 350  
Thr Ala Thr Ser Asn Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr  
80 85 90

cga aag aca cgc att gga ggc ctg cag gac caa gag tgc atc ccg tgc 398

A2  
Cm.t

Arg	Lys	Thr	Arg	Ile	Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys		
			95					100					105				
acg	aag	cag	acc	ccc	acc	tct	gag	gtt	caa	tgt	gcc	ttc	cag	ttg	agc	446	
Thr	Lys	Gln	Thr	Pro	Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser		
		110					115					120					
tta	gtg	gag	gca	gat	gca	ccc	aca	gtg	ccc	cct	cag	gag	gcc	aca	ctt	494	
Leu	Val	Glu	Ala	Asp	Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu		
	125					130					135						
gtt	gca	ctg	gtg	agc	agc	ctg	cta	gtg	gtg	ttt	acc	ctg	gcc	ttc	ctg	542	
Val	Ala	Leu	Val	Ser	Ser	Leu	Leu	Val	Val	Phe	Thr	Leu	Ala	Phe	Leu		
140					145					150					155		
ggg	ctc	ttc	ttc	ctc	tac	tgc	aag	cag	ttc	ttc	aac	aga	cat	tgc	cag	590	
Gly	Leu	Phe	Phe	Leu	Tyr	Cys	Lys	Gln	Phe	Phe	Asn	Arg	His	Cys	Gln		
				160					165					170			
cgt	gga	ggt	ttg	ctg	cag	ttt	gag	gct	gat	aaa	aca	gca	aag	gag	gaa	638	
Arg	Gly	Gly	Leu	Leu	Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu		
			175				180						185				
tct	ctc	ttc	ccc	gtg	cca	ccc	agc	aag	gag	acc	agt	gct	gag	tcc	caa	686	
Ser	Leu	Phe	Pro	Val	Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln		
		190					195					200					
gtc	tct	tgg	gcc	cct	ggc	agc	ctt	gcc	cag	ttg	ttc	tct	ctg	gac	tct	734	
Val	Ser	Trp	Ala	Pro	Gly	Ser	Leu	Ala	Gln	Leu	Phe	Ser	Leu	Asp	Ser		
	205				210						215						
gtt	cct	ata	cca	caa	cag	cag	cag	ggg	cct	gaa	atg	tgatgtccac				780	
Val	Pro	Ile	Pro	Gln	Gln	Gln	Gln	Gly	Pro	Glu	Met						
220				225				230									
angagcta	at	accctacaga	tg	ggggcatat	cctatcccat	cccaccagag	gattgattct	840									
ccatttcaca	aggactgac	tggagcattt	cttgccttccc	tg	ttgtagtc	tggggagcca	900										
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Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln	Trp	Gly	Arg	Cys	Val		
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Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly		
			20					25					30				
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg		
		35					40					45					
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys		

A2  
Cm.t

50

55

60

Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn  
65 70 75 80

Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile  
85 90 95

Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro  
100 105 110

Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp  
115 120 125

Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser  
130 135 140

Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu  
145 150 155 160

Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu  
165 170 175

Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val  
180 185 190

Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Trp Ala Pro  
195 200 205

Gly Ser Leu Ala Gln Leu Phe Ser Leu Asp Ser Val Pro Ile Pro Gln  
210 215 220

Gln Gln Gln Gly Pro Glu Met  
225 230

A2  
Cmcd.